

## SUPPLEMENTARY DATA

TABLE S1. Primers used for amplifying and sequencing.

Primer name	Direction	PCR, sequencing	Primer sequence 5'-3'	Source
<u><i>rps4 + spacer rps4-trnS</i></u>				
<i>rps4</i> -f	Forward	PCR,Seq	ATGTCCCGTTATCGAGGACCT	(Souza-Chies et al., 1997)
<i>trnS</i> -r	Reverse	PCR,Seq	TACCGAGGGTTCGAAC	(Souza-Chies et al., 1997)
<u><i>rps16</i> Intron</u>				
<i>rps16</i> -f	Forward	PCR,Seq	GTTGGTAGAAAGCAACGTGCGACTT	(Oxelman et al., 1997)
<i>rps16</i> -r2	Reverse	PCR,Seq	TCGGGATCGAACATCAATTGCAAC	(Oxelman et al., 1997)
<u><i>matK + matK-5' trnK</i> intron</u>				
<i>matK</i> -f1	Forward	PCR,Seq	ATGGAAGAATTACAAGGATAT	This study
<i>trnK</i> -2r	Reverse	PCR,Seq	AACTAGTCGGATGGAGTAG	(Johnston and Soltis, 1995)
<i>matK</i> -f2	Forward	Seq	CATATAAACCAATTATCAAAC	This study (internal primer)
<i>matK</i> -f3	Forward	Seq	CTTGTCTAAAGCTCAATTG	This study (internal primer)
<i>matK</i> -r1	Reverse	Seq	ATCCTGTACGATTGATACC	This study (internal primer)
<i>matK</i> -r2	Reverse	Seq	AGTTTGATAATTGGTTATAG	This study (internal primer)
<u><i>rbcL</i></u>				
<i>rbcL</i> -1f	Forward	PCR,Seq	ATGAGTTGTAGGGAGGGACT	(Reeves et al., 2001)
<i>rbcL</i> -1360r	Reverse	PCR,Seq	CTTCACAAGCAGCAGCTAGTTC	(Reeves et al., 2001)
<i>rbcL</i> -656f	Forward	Seq	TGCGTTGGAGAGACCCTTTC	This study (internal primer)
<i>rbcL</i> -675r	Reverse	Seq	GAAACGGTCTCTCCAACGC	This study (internal primer)
<u><i>trnL-F</i> region</u>				
c B49317	Forward	PCR,Seq	CGAAATCGGTAGACGCTACG	(Taberlet et al. 1991)
f A50272	Reverse	PCR,Seq	ATTGAACTGGTGACACGAG	(Taberlet et al. 1991)
e B49873	Forward	Seq	GGTTCAAGTCCCTCTATCCC	(Taberlet et al. 1991)
d A49855	Reverse	Seq	GGGGATAGAGGGACTTGAAC	(Taberlet et al. 1991)

Seq = sequencing

TABLE S2. PCR profiles for DNA amplification: (1) initial denaturation; (2) number of cycles; (3) denaturation, annealing, and elongation steps for each cycle; (4) final elongation step. Temperature and duration are indicated for each step.

Locus	PCR profiles
<i>rps4 + spacer rps4-trnS</i>	(1) 94°C-3 mn; (2) 40; (3) 94°C-1 mn, 56°C - 40 s, 72°C-1:30 mn; (4) 72°C-5 mn
<i>rps16</i> intron	(1) 94°C-3 mn; (2) 40; (3) 94°C-1 mn, 58°C - 40 s, 72°C-1:30 mn; (4) 72°C-5 mn
<i>matK + matK-5' trnK</i> intron	(1) 94°C-3 mn; (2) 40; (3) 94°C-1 mn, 53°C - 40 s, 72°C-2 mn; (4) 72°C-5 mn
<i>rbcL</i>	(1) 94°C-3 mn; (2) 40; (3) 94°C-1 mn, 55°C - 40 s, 72°C-2 mn; (4) 72°C-5 mn
<i>trnL-F</i> region	(1) 94°C-3 mn; (2) 40; (3) 94°C-1 mn, 56°C - 40 s, 72°C-1:40 mn; (4) 72°C-5 mn

TABLE S3. Data and models used in Maximum Likelihood (ML) and Bayesian analyses (BI).

Data partition	No. of positions (without primers)	Partition by codon position	Model	
			ML	BI
<b>DNA partition</b>				
Spacer <i>rps4-trnS</i>	378			GTR+G
<i>rps16</i> exon 2	42	X		K80
<i>rps16</i> intron	976			GTR+G
<i>matK</i>	1624	X		GTR+I+G
<i>matK</i> -5' <i>trnK</i> intron	309		GTRGAMMA	GTR+G
<i>rbcL</i>	1360	X		GTR+I+G
<i>trnL</i> intron	629			GTR+G
<i>trnL</i> exon 2	50			K80
Spacer <i>trnL-trnF</i>	477			GTR+G
<b>Coded indels partition (binary character)</b>				
Spacer <i>rps4-trnS</i>	62			
<i>rps16</i> intron	66		BINGAMMA	Simple model with variable rates
<i>matK</i> -5' <i>trnK</i> intron	73			
<i>trnL-F</i> region	129			

Partition by codon position = partition treated as a coding partition.

TABLE S4. Type and distribution of the floral glandular structures among the genera and species studied, arranged according to the classification of Goldblatt and Manning (2008).

Taxon	Floral glandular structure			Source
	Anatomical type	Secretory type	Distribution	
<b><i>Sisyrinchieae</i></b>				
<i>Libertia</i>	0	0	0	Goldblatt and Manning (2006, 2008)
<i>Olsynium douglasii</i>	4	5	1	Rudall et al. (2003), Chauveau et al. (2011)
<i>Olsynium filifolium</i>	Unknown	Unknown	Unknown	This study (presence of a swollen staminal colum, nectar presence not tested)
<i>Olsynium frigidum</i>	0	0	0	This study (absence of swollen staminal column)
<i>Olsynium junceum</i>	4	5	1	Forcone et al. (1998), Chauveau et al. (2011)
<i>Olsynium scirpoideum</i>	Unknown	Unknown	Unknown	Chauveau et al. (2011) / this study (presence of a swollen staminal colum, nectar presence not tested)
<i>Orthrosanthus</i>	0	0	0	Rudall et al. (2003), Goldblatt and Manning (2006, 2008), Chauveau et al. (2011)
<i>Sisyrinchium angustifolium</i>	1	0	0	Chauveau et al. (2011) and Silveiro, A., personal communication.
<i>Sisyrinchium californicum</i>	0	0	0	Chauveau et al. (2011)
<i>Sisyrinchium chilense</i>	1	2	1	Chauveau et al. (2011)
<i>Sisyrinchium convolutum</i>	0	0	0	Chauveau et al. (2011)
<i>Sisyrinchium micranthum</i>	1	2	1	Chauveau et al. (2011)
<i>Sisyrinchium minus</i>	1	2	1	Chauveau et al. (2011)
<i>Sisyrinchium palmifolium</i>	0	0	0	Chauveau et al. (2011)
<i>Sisyrinchium aff. pusillum</i>	0	0	0	Chauveau et al. (2011) / this study
<i>Sisyrinchium sellowianum</i>	1	2	1	Chauveau et al. (2011)
<i>Sisyrinchium striatum</i>	1	2	3	Chauveau et al. (2011)
<i>Sisyrinchium uliginosum</i>	1	2	1	Chauveau et al. (2011)
<i>Solenomelus pedunculatus</i>	1	0	1	Chauveau et al. (2011) and Silveiro, A., personal communication.
<i>Solenomelus segethii</i>	2	3	1	Chauveau et al. (2011) and Silveiro, A., personal communication.
<b><i>Trimezieae</i></b>				
<i>Neomarica candida</i>	1	1	2	Vogel (1974)
<i>Neomarica northiana</i>	1	1	2	Vogel (1974)
<i>Pseudotrimenia</i>	0	0	0	Chukr and Giulietti (2003), Goldblatt and Manning (2008)
<i>Trimezia</i>	1	2	2	Simpson and Neff (1981), Ravenna (1988), Goldblatt and Manning (2008)
<b><i>Tigridieae</i></b>				
<i>Ainea</i>	0	0	0	Ravenna (1979a)
<i>Alophia sylvestris</i>	1	2	2	Henrich and Goldblatt (1994), Goldblatt and Manning (2008)
<i>Alophia veracruzana</i>	0	0	0	Goldblatt and Howard (1992)
<i>Calydorea alba</i>	0	0	0	Roitman and Castillo (2005) / this study
<i>Calydorea approximata</i>	0	0	0	Goldblatt and Henrich (1991)
<i>Calydorea azurea</i>	0	0	0	Goldblatt and Henrich (1991)

<i>Calydorea basaltica</i>	0	0	0	Ravenna (2005) / this study (very few trichomes at the base of the adaxial face of tepals)
<i>Calydorea campestris</i>	0	0	0	Goldblatt and Henrich (1991) / this study (very few trichomes at the base of the adaxial face of tepals)
<i>Calydorea crocoides</i>	0	0	0	Goldblatt and Henrich (1991) / this study (very few trichomes at the base of the adaxial face of tepals)
<i>Calydorea longipes</i>	0	0	0	Ravenna (2005) / this study (very few trichomes at the base of the adaxial face of tepals)
<i>Calydorea minima</i>	0	0	0	Roitman and Castillo (2007)
<i>Calydorea pallens</i>	0	0	0	Goldblatt and Henrich (1991), Ravenna (2001)
<i>Calydorea undulata</i>	0	0	0	Ravenna (2001)
<i>Calydorea xyphioides</i>	0	0	0	Goldblatt and Manning (2008)
<i>Cardenanthus vargasii</i>	1	2	2	Goldblatt and Manning (2008) / this study
<i>Cardiostigma</i>	0	0	0	Foster (1945)
<i>Catila amabilis</i>	1	2	2	Ravenna (1983)
<i>Cipura campanulata</i>	0	0	0	Henrich and Goldblatt (1994)
<i>Cipura paludosa</i>	1	2	2	Henrich and Goldblatt (1994), (Goldblatt and Manning (2008)
<i>Cobana</i>	0	0	0	Ravenna (1974), Henrich and Goldblatt (1994), Goldblatt and manning (2008)
<i>Cypella</i>	1	2	2	Vogel (1974), Ravenna (1981a, 1981b), Goldblatt and Manning (2008)
<i>Eleutherine</i>	0	0	0	Goldblatt and Manning (2008)
<i>Ennealophus euryandrus</i>	1	2	2	Vogel (1974), Goldblatt and Manning (2008)
<i>Gelasine coerulea</i>	0	0	0	This study
<i>Gelasine elongata</i>	0	0	0	This study
<i>Herbertia</i>	1	2	3	Vogel (1974), Ravenna (1989), Goldblatt and Manning (2008)
<i>Hesperoxiphion</i>	1	2	2	Ravenna (1979b), Goldblatt and Manning (2008)
<i>Kelissa brasiliensis</i>	1	2	2	Ravenna (1981c)
<i>Larentia mexicana</i>	1	Unknown	2	Foster (1950), Espejo-Serna and Lopez-Ferrari (1996)
<i>Larentia rosei</i>	0	0	0	Espejo-Serna and Lopez-Ferrari (1996)
<i>Mastigostyla cyrtophylla</i>	0	0	0	This study
<i>Mastigostyla sp.01</i>	1	2	2	Goldblatt and Manning (2008) / this study
<i>Nemastylis</i>	0	0	0	Manning and Goldblatt (2008)
<i>Onira unguiculata</i>	1	2	2	Ravenna (1983)
<i>Phalocallis</i>	1	2	2	Ravenna (2009) / this study
<i>Sessilanthera</i>	0	0	0	Molseed and Cruden (1969), Goldblatt and Manning (2008)
<i>Tigridia philippiana</i>	1	2	2	Ravenna (1969) for <i>T. minuta</i> , Vogel (1974) for <i>T. lutea</i> / this study
<i>Tigridia</i> (subgenus <i>Tigridia</i> )	1	2	2	Molseed (1970), Goldblatt and Manning (2008)
<i>Tigridia</i> (subgenus <i>Hydrotaenia</i> )	1	1	2	Molseed (1970), Goldblatt and Manning (2008)
<i>Tigridia</i> ( <i>Rigidella</i> )	1	1	2	Cruden (1971), Goldblatt and Manning (2008)
<i>Tigridia</i> ( <i>Colima</i> )	1	1	2	Molseed and Cruden (1968), Goldblatt and Manning (2008)

Floral glandular structure. Anatomical type: (0) absent, (1) unicellular trichomes, (2) pluricellular scales, (3) carpel margin cells, (4) epithelial cells. Secretory type: (0) absent, (1) trichomal nectaries, (2) trichomal elaiophores, (3) pluricellular scales nectaries, (4) septal nectaries, (5) epithelial nectaries. Distribution: (0) absent, (1) staminal column, (2) inner tepals, (3) tepals, (4) ovary.

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TABLE S5. Comparison of full and constrained ML BISSE analyses. The six BISSE parameters are the speciation rates ( $\lambda_0$  and  $\lambda_1$ ) in absence vs. presence of glandular trichomes (character D) in the lineages, the extinction rates ( $\mu_0$  and  $\mu_1$ ), and forward and reverse transition rates ( $q_{01}$  and  $q_{10}$ ). Nested models were compared with likelihood ratio tests with 1 degree of freedom; the comparison is given in the comparison column.  $P$ -values are in bold when significant ( $P \leq 0.05$ ) and underlined when marginally significant.

Model	Constraints	$\lambda_0$	$\lambda_1$	$\mu_0$	$\mu_1$	$q_{01}$	$q_{10}$	$\ln L$	Comparison	$P$
D-1	None	128.54	261.79	77.82	84.59	71.82	148.54	-333.11		
D-2	$\lambda_0 = \lambda_1$	213.06	213.06	219.03	2.97 E-5	52.42	187.58	-332.10	vs. D-1	0.155
D-3	$\mu_0 = \mu_1$	129.36	259.83	80.33	80.33	70.62	149.50	-333.11	vs. D-1	0.975
D-4	$q_{10} = q_{01}$	112.66	317.31	6.40	210.23	126.74	126.74	-332.72	vs. D-1	0.378
D-5	$\lambda_0 = \lambda_1, \mu_0 = \mu_1$	215.25	215.25	123.28	123.28	125.47	155.49	-329.79	vs. D-3	<b>0.009</b>
D-6	$\lambda_0 = \lambda_1, q_{10} = q_{01}$	215.16	215.16	132.12	114.67	162.05	162.05	-329.53	vs. D-3	<b>0.007</b>
D-7	$\mu_0 = \mu_1, q_{10} = q_{01}$	155.01	251.21	111.71	111.71	173.86	173.86	-330.99	vs. D-3	<b>0.039</b>

  

Model	Constraints	$\lambda_0$	$\lambda_1$	$\mu_0$	$\mu_1$	$q_{01}$	$q_{10}$	$\ln L$	Comparison	$P$
D-8	$\lambda_0 = \lambda_1, \mu_0 = \mu_1, q_{10} = q_{01}$	215.25	215.25	123.28	123.28	158.32	158.32	-329.50		
D-7	$\mu_0 = \mu_1, q_{10} = q_{01}$	155.01	251.21	111.71	111.71	173.86	173.86	-330.99	vs. D-8	<u>0.0840</u>
D-6	$\lambda_0 = \lambda_1, q_{10} = q_{01}$	215.16	215.16	132.12	114.67	162.05	162.05	-329.53	vs. D-8	0.8064
D-5	$\lambda_0 = \lambda_1, \mu_0 = \mu_1$	215.25	215.25	123.28	123.28	125.47	155.49	-329.79	vs. D-8	0.4463
D-4	$q_{10} = q_{01}$	112.66	317.31	6.40	210.23	126.74	126.74	-332.72	vs. D-7	0.0628
D-3	$\mu_0 = \mu_1$	129.36	259.83	80.33	80.33	70.62	149.50	-333.11	vs. D-7	<b>0.0394</b>

TABLE S6. Comparison of full and constrained ML BISSE analyses. The six BISSE parameters are the speciation rates ( $\lambda_0$  and  $\lambda_1$ ) in absence vs. presence of trichomal elaiophores (character E) in the lineages, the extinction rates ( $\mu_0$  and  $\mu_1$ ), and forward and reverse transition rates ( $q_{01}$  and  $q_{10}$ ). Nested models were compared with likelihood ratio tests with 1 degree of freedom; the comparison is given in the comparison column. *P*-values are bolded when significant ( $P \leq 0.05$ ) and underlined when marginally significant.

Model	Constraints	$\lambda_0$	$\lambda_1$	$\mu_0$	$\mu_1$	$q_{01}$	$q_{10}$	ln L	Comparison	<i>P</i>
E-1	None	190.92	231.14	161.63	29.26	86.91	252.58	-331.16		
E-2	$\lambda_0 = \lambda_1$	212.02	212.02	191.51	7.00 E-5	82.20	259.62	-331.09	vs. E-1	0.713
E-3	$\mu_0 = \mu_1$	179.48	260.20	116.63	116.63	102.40	214.43	-331.08	vs. E-1	0.690
E-4	$q_{10} = q_{01}$	168.18	309.26	31.46	275.47	155.57	155.57	-330.44	vs. E-1	0.229
E-5	$\lambda_0 = \lambda_1, \mu_0 = \mu_1$	215.25	215.25	123.28	123.28	126.40	208.21	-330.41	vs. E-2	0.243
E-6	$\lambda_0 = \lambda_1, q_{10} = q_{01}$	213.67	213.67	72.86	188.06	177.18	177.18	-329.50	vs. E-2	0.074
E-7	$\mu_0 = \mu_1, q_{10} = q_{01}$	223.06	205.13	122.60	122.60	171.45	171.45	-328.57	vs. E-2	<b>0.024</b>
E-8	$\lambda_0 = \lambda_1, \mu_0 = \mu_1, q_{10} = q_{01}$	215.25	215.25	123.28	123.28	168.40	168.40	-328.53	vs. E-5	<u>0.052</u>

Model	Constraints	$\lambda_0$	$\lambda_1$	$\mu_0$	$\mu_1$	$q_{01}$	$q_{10}$	ln L	Comparison	<i>P</i>
E-8	$\lambda_0 = \lambda_1, \mu_0 = \mu_1, q_{10} = q_{01}$	215.25	215.25	123.28	123.28	168.40	168.40	-328.53		
E-7	$\mu_0 = \mu_1, q_{10} = q_{01}$	223.06	205.13	122.60	122.60	171.45	171.45	-328.57	vs. E-8	0.7772
E-6	$\lambda_0 = \lambda_1, q_{10} = q_{01}$	213.67	213.67	72.86	188.06	177.18	177.18	-329.50	vs. E-8	0.1636
E-5	$\lambda_0 = \lambda_1, \mu_0 = \mu_1$	215.25	215.25	123.28	123.28	126.40	208.21	-330.41	vs. E-8	<u>0.0524</u>
E-4	$q_{10} = q_{01}$	168.18	309.26	31.46	275.47	155.57	155.57	-330.44	vs. E-5	0.8064
E-3	$\mu_0 = \mu_1$	179.48	260.20	116.63	116.63	102.40	214.43	-331.08	vs. E-5	0.2470
E-2	$\lambda_0 = \lambda_1$	212.02	212.02	191.51	7.00 E-5	82.20	259.62	-331.09	vs. E-5	0.2435

TABLE S7. Detection of diversification rate variations among the tribes Sisyrinchieae, Trimezieae and Tigridieae using the SymmeTREE software. Uncertainties associated with polytomies within the strict consensus tree (MP analysis) and the 50 % majority rule (MR) consensus tree (Bayesian analysis) were assessed by generating 100 000 random resolutions under the TSS ERM algorithm, providing upper and lower bounds on the confidence interval. These 'high' and 'low' asymmetry values correspond to the tail probabilities for the .025 and .975 frequentiles, respectively. The sensitivity of the whole-tree statistics to large-scale diversification rate variation decreases to the right across a given row (i.e.,  $I_c > M_\pi^* > M_\pi > M_\Sigma^* > M_\Sigma > B_1$ ).

Fully resolved tree	$I_c$	$M_\pi^*$	$M_\pi$	$M_\Sigma^*$	$M_\Sigma$	$B_1$
<b>ML best-scoring tree</b>	0.09759	<u>0.02394</u>	<u>0.01775</u>	<u>0.00904</u>	<u>0.0211</u>	0.20651
<b>Tree with polytomies</b>	$I_c$	$M_\pi^*$	$M_\pi$	$M_\Sigma^*$	$M_\Sigma$	$B_1$
	high	high	high	high	high	high
	low	low	low	low	low	low
<b>Strict consensus tree</b>	0.10084	<u>0.02631</u>	<u>0.01705</u>	<u>0.00893</u>	<u>0.0136</u>	0.10804
<b>(MP)</b>	0.26363	0.18538	0.19139	0.13653	0.19749	0.53232
<b>MR consensus tree</b>	0.101	<u>0.02637</u>	<u>0.01493</u>	<u>0.00668</u>	<u>0.0105</u>	0.0916
<b>(Bayesian analysis)</b>	0.36135	0.27515	0.23865	0.19169	0.20363	0.44118

Significant  $P$ -values are underlined.